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New Enhancer-Gene Map

About PANTHER Data PANTHER Tools PANTHER Services Workspace Downloads PANTHER16.0 Released.

Analysis Summary: Please report in publication ②

Analysis Type: PANTHER Overrepresentation Test (Released 20210224) Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.4495804 Released 2021-02-01 Analyzed List: genes_for_GO_FST_VIABILITY_TOP1_genotyped.tsv (Homo sapiens) Change Reference List: universe_genotyped.tsv (Homo sapiens) Change **▽** ? Annotation Data Set: GO biological process complete Test Type: ● Fisher's Exact ○ Binomial

Correction: O Calculate False Discovery Rate Use the Bonferroni correction for multiple testing O No correction

Results ? Reference list Uniquely Mapped IDS: 17122 out of 17137

genes_for_GO_FST_VIABILITY_TOP1_genotyped.tsv

1918 out of 1961

Unmapped IDs: <u>15863</u> <u>1964</u> Multiple mapping 1243 <u>41</u> information:

Export Table XML with user input ids JSON with user input ids

Displaying only results for FDR P < 0.05, <u>click here to display all results</u>

	universe_genotyped.tsv (REF)	genes	for GO FST	VIABILITY_TOP1_g	<u>jenotype</u>	<u>ed.tsv</u> (<u>▼ Hierar</u>	chy_NEW! ③)
GO biological process complete	<u>#</u>	<u>#</u>	<u>expected</u>	Fold Enrichment	+/-	raw P value	<u>FDR</u>
glutamate receptor signaling pathway	43	<u>16</u>	4.92	3.25	+	2.15E-04	3.60E-02
<u> </u>	4770	<u>635</u>	545.83	1.16	+	2.87E-05	6.68E-03
<u> Gellular process</u>	<u>13510</u>	<u>1615</u>	1545.96	1.04	+	2.40E-04	3.89E-02
<u> </u>	4844	<u>640</u>	554.30	1.15	+	6.16E-05	1.28E-02
<u> •regulation of cellular process</u>	<u>9853</u>	<u>1230</u>	1127.49	1.09	+	8.71E-06	2.95E-03
<u> </u>	<u>10340</u>	<u>1279</u>	1183.21	1.08	+	2.64E-05	6.23E-03
<u> </u>	<u>10963</u>	<u>1358</u>	1254.50	1.08	+	3.14E-06	1.26E-03
neuron recognition	<u>46</u>	<u>17</u>	5.26	3.23	+	1.48E-04	2.67E-02
<u> heuron development</u>	<u>774</u>	<u>160</u>	88.57	1.81	+	4.73E-11	2.46E-07
<u> </u>	<u>1492</u>	<u>255</u>	170.73	1.49	+	2.31E-09	3.27E-06
<u> </u>	<u>3190</u>	<u>450</u>	365.03	1.23	+	5.99E-06	2.12E-03
<u> </u>	3239	<u>457</u>	370.64	1.23	+	4.44E-06	1.65E-03
4developmental process	<u>5180</u>	<u>682</u>	592.75	1.15	+	4.39E-05	9.63E-03
-anatomical structure development	<u>4781</u>	<u>648</u>	547.09	1.18	+	2.50E-06	1.02E-03
<u> •neuron differentiation</u>	949	<u>185</u>	108.59	1.70	+	1.10E-10	3.42E-07
□generation of neurons	<u>1154</u>	217	132.05	1.64	+	3.16E-11	2.46E-07
<u> </u>	<u>1267</u>	<u>235</u>	144.98	1.62	+	1.73E-11	2.70E-07
<u> </u>	<u>2006</u>	330	229.55	1.44	+	3.41E-10	7.59E-07
<u> </u>	<u>3902</u>	<u>548</u>	446.51	1.23	+	5.03E-07	2.70E-04
4multicellular organism development	4441	<u>610</u>	508.19	1.20	+	1.13E-06	5.66E-04
dendrite morphogenesis	<u>53</u>	<u>18</u>	6.06	2.97	+	2.25E-04	3.74E-02
4cell morphogenesis involved in neuron differentiation	417	<u>94</u>	47.72	1.97	+	2.02E-08	1.75E-05
4-cell morphogenesis involved in differentiation	<u>512</u>	<u>106</u>	58.59	1.81	+	1.14E-07	7.72E-05
<u> </u>	<u>659</u>	<u>134</u>	75.41	1.78	+	5.11E-09	6.12E-06
<u> </u>	<u>1979</u>	308	226.46	1.36	+	2.12E-07	1.27E-04
4-dendrite development	98	<u>29</u>	11.21	2.59	+	4.37E-05	9.73E-03
-neuron projection development	<u>634</u>	<u>129</u>	72.55	1.78	+	1.13E-08	1.04E-05
uplasma membrane bounded cell projection organization	<u>1084</u>	<u>183</u>	124.04	1.48	+	1.23E-06	5.99E-04
<u> </u>	<u>1124</u>	<u>187</u>	128.62	1.45	+	2.27E-06	9.54E-04
<u> </u>	<u>5079</u>	<u>678</u>	581.19	1.17	+	8.78E-06	2.91E-03
4cellular component organization or biogenesis	<u>5278</u>	<u>688</u>	603.97	1.14	+	1.26E-04	2.42E-02
<u> </u>	<u>462</u>	<u>103</u>	52.87	1.95	+	5.62E-09	5.83E-06
□ plasma membrane bounded cell projection morphogenesis	<u>466</u>	<u>104</u>	53.32	1.95	+	6.09E-09	5.93E-06
4cell projection morphogenesis	<u>469</u>	<u>105</u>	53.67	1.96	+	4.47E-09	5.80E-06
<u> </u>	486	<u>107</u>	55.61	1.92	+	5.38E-09	5.99E-06
<u> </u>	<u>566</u>	<u>115</u>	64.77	1.78	+	7.42E-08	5.26E-05
regulation of synapse assembly	86	<u>26</u>	9.84	2.64	+	5.80E-05	1.24E-02

1/3 pantherdb.org/tools/compareToRefList.jsp

22/04/2021	PANTHER - Compare list	ts to reference l	ist				
<u> </u>	<u>190</u>	<u>42</u>	21.74	1.93	+	2.78E-04	4.46E-02
<u> </u>	<u>2180</u>	<u>311</u>	249.46	1.25	+	1.31E-04	2.42E-02
<u> </u>	<u>201</u>	<u>45</u>	23.00	1.96	+	1.19E-04	2.32E-02
<u> </u>	<u>3668</u>	<u>520</u>	419.73	1.24	+	3.84E-07	2.14E-04
synapse organization	<u>254</u>	<u>66</u>	29.07	2.27	+	3.87E-08	3.02E-05
<u> </u>	<u>460</u>	99	52.64	1.88	+	5.66E-08	4.20E-05
axon guidance	<u>260</u>	<u>65</u>	29.75	2.18	+	1.48E-07	9.62E-05
<u> </u>	<u>261</u>	<u>65</u>	29.87	2.18	+	1.58E-07	9.82E-05
<u> </u>	<u>1177</u>	<u>191</u>	134.69	1.42	+	7.00E-06	2.42E-03
<u> →movement of cell or subcellular component</u>	<u>1421</u>	240	162.61	1.48	+	2.09E-08	1.71E-05
<u> </u>	<u>357</u>	<u>79</u>	40.85	1.93	+	5.52E-07	2.87E-04
<u> axon development</u>	<u>389</u>	<u>80</u>	44.51	1.80	+	4.76E-06	1.72E-03
cell-cell adhesion via plasma-membrane adhesion molecules	<u>240</u>	<u>52</u>	27.46	1.89	+	8.47E-05	1.71E-02
<u> </u>	<u>476</u>	99	54.47	1.82	+	2.74E-07	1.58E-04
<u> </u>	<u>884</u>	<u>176</u>	101.16	1.74	+	7.64E-11	2.98E-07
⁴ biological adhesion	<u>889</u>	<u>176</u>	101.73	1.73	+	1.20E-10	3.12E-07
regulation of transporter activity	<u>260</u>	<u>54</u>	29.75	1.82	+	1.54E-04	2.76E-02
<u> </u>	<u>2872</u>	<u>403</u>	328.65	1.23	+	3.86E-05	8.72E-03
extracellular matrix organization	<u>364</u>	<u>75</u>	41.65	1.80	+	1.01E-05	3.16E-03
<u> </u>	<u>365</u>	<u>75</u>	41.77	1.80	+	1.05E-05	3.21E-03
<u> </u>	<u>367</u>	<u>75</u>	42.00	1.79	+	1.14E-05	3.30E-03
modulation of chemical synaptic transmission	<u>402</u>	<u>81</u>	46.00	1.76	+	9.05E-06	2.94E-03
<u> </u>	<u>403</u>	<u>81</u>	46.12	1.76	+	9.36E-06	2.98E-03
<u> </u>	<u>3133</u>	<u>471</u>	358.51	1.31	+	2.20E-09	3.42E-06
<u> </u>	<u>3166</u>	<u>477</u>	362.29	1.32	+	1.21E-09	2.35E-06
regulation of neuron projection development	<u>413</u>	<u>82</u>	47.26	1.74	+	1.19E-05	3.37E-03
regulation of plasma membrane bounded cell projection organization	<u>582</u>	<u>111</u>	66.60	1.67	+	2.05E-06	8.87E-04
<u> </u>	<u>598</u>	<u>114</u>	68.43	1.67	+	1.48E-06	6.79E-04
regulation of GTPase activity	438	<u>86</u>	50.12	1.72	+	1.06E-05	3.17E-03
<u> </u>	<u>1181</u>	<u>182</u>	135.14	1.35	+	1.71E-04	3.00E-02
<u> </u>	<u>2287</u>	<u>321</u>	261.70	1.23	+	3.02E-04	4.76E-02
positive regulation of cell adhesion	<u>409</u>	<u>77</u>	46.80	1.65	+	1.06E-04	2.08E-02
<u> </u>	<u>681</u>	<u>121</u>	77.93	1.55	+	1.32E-05	3.54E-03
<u> </u>	<u>5050</u>	<u>672</u>	577.88	1.16	+	1.37E-05	3.57E-03
<u> </u>	<u>5544</u>	<u>730</u>	634.40	1.15	+	1.59E-05	3.99E-03
trans-synaptic signaling	<u>402</u>	<u>75</u>	46.00	1.63	+	1.70E-04	3.01E-02
<u> </u>	<u>426</u>	<u>79</u>	48.75	1.62	+	1.40E-04	2.56E-02
regulation of membrane potential	<u>404</u>	<u>74</u>	46.23	1.60	+	3.15E-04	4.86E-02
regulation of ion transmembrane transport	<u>530</u>	<u>96</u>	60.65	1.58	+	5.53E-05	1.20E-02
<u> </u>	<u>1240</u>	<u>189</u>	141.89	1.33	+	2.00E-04	3.42E-02
<u> </u>	<u>1636</u>	247	187.21	1.32	+	3.12E-05	7.15E-03
<u> </u>	<u>2536</u>	<u>395</u>	290.20	1.36	+	1.96E-09	3.40E-06
<u> </u>	<u>535</u>	<u>97</u>	61.22	1.58	+	5.82E-05	1.23E-02
regulation of cell migration	<u>814</u>	<u>140</u>	93.15	1.50	+	1.13E-05	3.31E-03
<u> </u>	<u>872</u>	<u>148</u>	99.78	1.48	+	1.28E-05	3.56E-03
<u> </u>	949	<u>162</u>	108.59	1.49	+	3.31E-06	1.29E-03
<u> </u>	<u>915</u>	<u>152</u>	104.70	1.45	+	2.48E-05	5.95E-03
tube morphogenesis	<u>600</u>	<u>102</u>	68.66	1.49	+	2.92E-04	4.64E-02
regulation of anatomical structure morphogenesis	<u>882</u>	<u>148</u>	100.93	1.47	+	2.27E-05	5.60E-03
<u> </u>	<u>2237</u>	332	255.98	1.30	+	3.85E-06	1.46E-03
regulation of protein localization	<u>839</u>	<u>136</u>	96.01	1.42	+	1.81E-04	3.13E-02
positive regulation of developmental process	<u>1167</u>	<u>179</u>	133.54	1.34	+	2.29E-04	3.76E-02
positive regulation of molecular function	<u>1612</u>	<u>239</u>	184.46	1.30	+	1.27E-04	2.41E-02
regulation of signal transduction	<u>2778</u>	403	317.89	1.27	+	1.82E-06	8.10E-04
<u> </u>	<u>3741</u>	<u>524</u>	428.09	1.22	+	1.29E-06	6.09E-04
detection of chemical stimulus involved in sensory perception of smell	<u>344</u>	<u>14</u>	39.36	.36	-	1.34E-05	3.53E-03
<u> </u>	<u>384</u>	<u>17</u>	43.94	.39	-	1.28E-05	3.51E-03
<u> detection of chemical stimulus</u>	<u>419</u>	<u>20</u>	47.95	.42	-	1.53E-05	3.90E-03
<u> </u>	<u>436</u>	<u>23</u>	49.89	.46	-	6.42E-05	1.32E-02
4sensory perception of smell	<u>369</u>	<u>18</u>	42.22	.43	-	8.72E-05	1.74E-02
mitochondrial translational termination	<u>82</u>	<u>0</u>	9.38	< 0.01	-	3.19E-04	4.87E-02
4translational termination	<u>88</u>	<u>0</u>	10.07	< 0.01	-	1.30E-04	2.45E-02
<u> →mitochondrial translation</u>	<u>103</u>	<u>0</u>	11.79	< 0.01	-	2.48E-05	6.04E-03
<u></u> <u>→mitochondrial gene expression</u>	<u>128</u>	2	14.65	.14	-	2.06E-04	3.49E-02
mitochondrial translational elongation	<u>81</u>	<u>0</u>	9.27	< 0.01	-	3.04E-04	4.74E-02

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